In the specification:

Insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

Replace the paragraph beginning at page 7, line 3 with the following rewritten paragraph:

Figure 1 is a summary of NMR-derived secondary structure indicators measured for TNFR-DD R347A together with the deduced secondary structure. For NOE data, the thickness of the lines reflects strength of sequential NOEs. The amino acid sequence is also shown (SEQ ID NO:1).

Replace the paragraph beginning at page 7, line 14 with the following rewritten paragraph:

Figure 4 represents a sequence alignment of the death domains of TNFR-1 (SEQ ID NO:8) and Fas (SEQ ID NO:9). The helices in the NMR structure of the TNFR-1 and Fas (Huang et al., 1996) are indicated. The mutations are indicated by an arrow pointing to the amino acid of substitution. A minus sign above the TNFR-1 mutation indicates a loss in self-association or interaction with TRADD-DD (see text). A minus sign below the Fas mutation indicates that this mutant aggregates less than the wild-type protein (Huang et al., 1996).

Replace the paragraph beginning at page 7, line 28 with the following rewritten paragraph:

Figure 6 depicts a summary of H-D exchange, $^{3}J_{HNH\alpha}$ scalar coupling information, sequential NOEs ($d_{\alpha N}$, d_{NN}, $d_{\beta N}$), medium range NOEs ($d_{NN(i,i+2)}$, $d_{\alpha N(i,i+3)}$, $d_{\alpha N(i,i+4)}$, $d_{\alpha\beta(i,i+3)}$), and the $\Delta^{13}C_{\alpha}$ and $\Delta^{13}C_{\beta}$. Amides that didn't exchange with D_2O within 30 minutes are designated with an (∘). The residues having a $^{3}J_{HNH\alpha}$ less than 5 Hz are designated with an solid line. The intensities of the NOEs are represented by the thickness of the lines. The values of the $\Delta^{13}C_{\alpha}$ and $\Delta^{13}C_{\beta}$ are represented by the intensity of the blocks. The secondary structure highlighting the 6 α-helices is indicated at the bottom. The amino acid sequence is also shown (SEQ ID NO:1).

Replace the paragraph beginning at page 8, line 7 with the following rewritten paragraph:

Figure 7 depicts the secondary structure and sequence alignment of TNFR-1 DD (SEQ ID NO:1) with proteins in the death domain superfamily (SEQ ID NOs 2-7), respectively. In instances when the lengths of the helices differed when compared to TNFR-1 DD, the sequences were aligned based upon sequence homology instead of secondary structure alignment.